SEQUENCE LISTING

<110> H. Robert Horvi

<120> A TUMOR SUPPRESSOR PATHWAY IN C. ELEGANS

<130> 01997/202002

<140> 09/087,136
<141> 1998-05-28

<150> 60/047,996
<151> 1997-05-28

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 275
<212> PRT
<213> Caenorhabditis elegans

<400> 1

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Pro Leu Glu Ser Pro Ser Arg Lys Leu Thr Ser Leu Leu Ser Tyr Asp
        35                  40                  45
Pro Thr Val Pro Glu Ser Pro Asp Met Lys Phe Ala Arg Lys Arg Leu
    50                  55                  60
Gly Asn Leu Leu Thr Thr Ile Lys His His Pro Ser Glu Ile Ile Gly
65                  70                  75                  80
Val Leu Pro Glu Asp Tyr Thr Arg Ala Asp Glu Glu Pro Gly Arg Gln
                85                  90                  95
Gly Arg Pro Pro Gly Arg Pro Arg Lys Met Pro Arg His Glu Ser Ser
            100                 105                 110
Thr Ser Leu Met Glu Ser Pro Arg Lys Thr Met Thr Arg Asp Ser Lys
        115                 120                 125
Ile Met Phe Glu Leu Arg Gly Lys Pro Phe Glu Met Ile Ala Gly Arg
    130                 135                 140
Phe Glu Glu Glu Tyr Ser Leu Gly Arg Ala Trp Val Lys Gly His Met
145                 150                 155                 160
Asn Asn Glu Tyr Glu Pro Ile Lys Ala Gln Arg Thr Asp Tyr Ala Pro
                165                 170                 175
Asn Leu Ala Val Asp Tyr Leu Ala Cys Arg Glu Ile His Arg Met Pro
            180                 185                 190
Arg Pro Asp Lys Ser Ile Pro Glu Leu Pro Ile Val Pro Ser Arg Ile
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        195                 200                 205
Asp Glu Phe Asp Ala Thr Val Asp Pro Arg Tyr Glu Thr Asp Leu Lys
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Asn Glu Tyr Ile Arg His Trp Lys Gln Val Lys Lys Gly Trp Cys Ala
225                 230                 235                 240
His Gln Arg Arg Arg Thr Ala Pro His Ala Arg Ser Ile Ala Leu Ile
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Asn Lys Ile Tyr Gln Pro Gly Glu Ser Lys Thr Val Glu Gln Ala Leu
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Gly Leu Ile
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<210> 2
<211> 954
<212> DNA
<213> Caenorhabditis elegans

<400> 2

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ctcacatccc tgttatccta tgatccgaca gttccggagt caccggatat gaaattcgcc     180
agaaaacgtc tgggaaatct gctgacaacc ataaaacatc acccatcgga aataattgga     240
gtactcccag aagattatac tcgtgctgat gaagagcccg ggcgccaagg acgtccacca     300
ggtcgccctc gtaagatgcc gcgtcacgaa tcttcaactt cacttatgga atcaccacgc     360
aagactatga ctcgtgattc taaaattatg tttgaattgc gtggaaaacc attcgaaatg     420
atagctggac gttttgaaga agaatattca cttggtagag catgggttaa aggacacatg     480
aataatgaat atgaaccaat aaaagctcaa aggacagact atgcaccgaa tctggctgtt     540
gattatcttg catgtcgcga gattcatcga atgccacgtc cagataaatc aattcctgag     600
ctgccaattg ttccatctag aatcgatgaa ttcgacgcta cagtcgatcc aagatatgaa     660
acagatttga aaaatgaata cattcgtcat tggaaacaag tcaaaaaagg ttggtgtgct     720
catcaacgtc gtcggactgc tccccatgca agaagcatag cattaatcaa caaaatctac     780
cagcctggag agtcgaaaac tgtcgagcaa gcacttggtc ttatttaaat attctaacat     840
gtaatttcaa tttatctctt actttctgat cttgctatca catgtctctt atttcaaaaa     900
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<210> 3
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<212> PRT
<213> Caenorhabditis elegans

<400> 3

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            20                  25                  30
Thr Asp Thr Ile Cys Glu Glu Pro Pro Ala Lys Arg Ile Asp Leu Asp
        35                  40                  45
Ile Lys Gln Glu Phe Asn Gly Gly Val Gln Ser Gly Gly Leu Ile Lys
    50                  55                  60
Asn Glu Ser Glu Leu Thr Gln Met Thr Ile Lys Gln Glu Thr Glu Gly
65                  70                  75                  80
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Asn Ile Asn Glu Ala Arg Arg Glu Glu Glu Asp Glu Glu Gln Asp Glu
                85                  90                  95
Asp Ser Arg Thr Ser Met Pro Pro Ala Leu Gly Glu Asp Asp Asp Tyr
            100                 105                 110
Glu Glu Asp Asp Ala Asp Ser Phe Ile Asp Lys Thr Asn Thr Pro Pro
        115                 120                 125
Pro Ser Gln Ser Phe Leu Glu Gly Cys Arg Ala Ala Asn Leu Pro Asn
    130                 135                 140
Asp Ile Val Thr Gly Ala Trp Glu Thr Tyr Asn His Ala Val Gln Arg
145                 150                 155                 160
Val Ser Leu Glu Gly Ser Glu Ser Ala Trp Gln Leu Ser Ala Ile Tyr
                165                 170                 175
Tyr Tyr Leu Leu Ser Lys Gly Ile Lys Arg Arg Gly Lys Thr Ile Arg
            180                 185                 190
Ile Leu Ile Gln Pro Phe Pro Val Ser Ile Leu Thr Ile Ala Asn Ser
        195                 200                 205
Phe Asp Ile Ser Val Ala Glu Met Leu Asp Lys Thr Ala Arg Phe Val
    210                 215                 220
Glu Ile Ile His Ser Arg Lys Ile Arg Arg Tyr Gln Glu Tyr Ile Arg
225                 230                 235                 240
Arg Ile Gln Glu Gly Leu Ala Val Ser Cys Val Ile Phe Lys Lys Phe
                245                 250                 255
Cys Arg Ile Phe Cys Lys Ile Phe Glu Glu Ile Lys Val Gly Ser Glu
            260                 265                 270
Asn Cys Pro Ser Ser His Glu Leu Phe Thr Val Leu Trp Thr Ser Phe
        275                 280                 285
Leu Val Met Lys Ser Arg Met Thr Val Asp Asp Leu Ile Ser Asn Tyr
    290                 295                 300
Gln Leu Leu Phe Ser Ile Leu Asp Gln Val Tyr Thr Glu Met Cys Ser
305                 310                 315                 320
Met Lys Glu Gly Ile Val His His Leu Asn Gln Lys Phe Val Glu Asp
                325                 330                 335
Leu Leu Glu Asn Asp Cys Thr Ile Ile Arg Ala Leu Cys Thr Gln Phe
            340                 345                 350
Gly Gly Ser Val Leu Asp Ala Arg His Phe Ser Asp His Thr Phe Lys
        355                 360                 365
Lys Met Glu Lys Thr Gly Ile Pro Ser Thr Trp Asn Phe Gln Glu Phe
    370                 375                 380
Arg Asp Leu Ile Met Asn Val Pro Lys Thr Ala Tyr Glu Asn Tyr Leu
385                 390                 395                 400
Leu Gln Arg Gly Ser Ile Asp Glu Arg Ile Phe Ile Pro Ser Val Glu
                405                 410                 415
Asp Phe Ser Lys Ile Phe Gln Ser Pro Asp Thr Tyr Ser Val Ala Asp
            420                 425                 430
Ile Leu Lys Val Ser Tyr Ser Gly Arg Arg Phe Arg Asp Ala Glu Phe
        435                 440                 445
Leu Thr Lys Ile Ser Asn Asn His Cys Leu Glu Lys Leu Ala Leu Gly
    450                 455                 460
Gly Lys Val Ala Ser Glu Lys Leu Val Thr Gln Ser Lys Glu Gln Pro
465                 470                 475                 480
Arg Val Pro Cys Val Glu Tyr Asn Leu Glu Leu Gly Asn Tyr Pro Asp
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485 490 495
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500 505 510
Ile Gly Ser Trp Lys Leu Glu Asn Ser Lys Leu Glu Glu Val Cys Gly
515 520 525
Thr Met Ser Asp Ser Pro Met Ala Thr Ile Leu Leu Lys Ser Asp Glu
530 535 540
Met Thr Asn Lys Phe Glu Arg Thr Leu Ser Ala Glu Leu Gly Glu Thr
545 550 555 560
Ile Asn Glu Asn Ile Pro Lys Tyr His Tyr Asn Val Arg Lys Glu Leu
565 570 575
Glu Leu Val Phe Leu Ile Phe Met Glu Lys Ile Ile Val Ala Glu Leu
580 585 590
Lys Lys Lys Val Arg Glu Glu Asp Leu Leu Asn Val Ile Arg Arg Glu
595 600 605
Glu Phe Leu Asp Ser Val Phe Cys Phe Cys Val Glu Leu Ile Leu Val
610 615 620
Ser Asn Gly Tyr Asp Arg Pro Phe Pro Trp Ser Ala Glu Leu Cys Gly
625 630 635 640
Val His Pro Phe Met Phe His Lys Val Ile Asp Leu Met Ile Thr His
645 650 655
Glu Lys Gln Leu Ser Arg Gln Met Val Gln His Phe Ser Arg Ile Glu
660 665 670
Glu Thr Val Ile Glu Tyr Phe Ser Trp Lys Ser Asp Ser Pro Leu Trp
675 680 685
Pro Met Val Val Arg Cys Pro Phe Ala His Phe Gln Glu Phe Gly Glu
690 695 700
Asp Trp Ala Asp Lys Leu Asn Ser Tyr Ser Pro Ile Lys Phe Thr Pro
705 710 715 720
Ile Lys Lys Pro Asp Asp Leu Arg Asp Glu Leu Gly Arg Pro Ile Val
725 730 735
Pro Gln Asn Gln Thr Ser Arg Thr Leu Arg Ile Phe Leu Lys Arg Thr
740 745 750
Tyr Phe Thr Ala Ala Arg Arg Leu Gln Asp Leu Thr Asp Arg Val Ser
755 760 765
Met Gly Ala Arg Ala Lys Ser Gln Cys Trp Ser Leu Phe Asp Tyr Leu
770 775 780
Leu Arg Asn Asp Thr Leu Ile Phe Met Asp Arg His Leu Asp Gln Ile
785 790 795 800
Leu Leu Cys Cys Val Phe Val Ile Met Lys Ile Asn Glu Ser Ser Met
805 810 815
Leu Phe Thr Glu Ile Met Ala Gln Tyr Arg Arg Gln Ser Ala Asn Ser
820 825 830
Leu Leu Val Tyr Arg Ser Val Thr Val Phe Gln Glu Gln Leu Asn Pro
835 840 845
Glu Asn Pro Gln Ala Val Asn Thr Lys Glu Thr Ile Leu Glu Arg Leu
850 855 860
Glu Gly Pro Gln Lys Glu Lys Thr Thr Val Asp Ile Ile Lys Tyr Tyr
865 870 875 880
Asn Ile Glu Phe Arg Asp Arg Ile Lys Tyr Ile Ile Gly Gln Ile Asp
885 890 895

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Ser Ala Ser Asp Glu Asp Leu Met Glu Met Pro Val Ala Thr Glu Ser
            900                 905                 910
Gly Leu Met Pro Val Arg Val Tyr Leu Thr His Lys Leu Ser Ile Gln
        915                 920                 925
Thr Leu Pro Lys Thr Lys His Gly Glu Ser Lys Gln Glu Arg Ala Ile
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Ala Asn Leu Glu Lys Ser Gly Ile Thr Ile Ala Met Glu Arg Ser Gly
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Asp
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<210> 4
<211> 3209
<212> DNA
<213> Caenorhabditis elegans

<400> 4

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ccagcaaaac gaatcgactt agatataaag caagaattca atggtggagt gcaaagtgga     180
gggctgatta aaaatgaatc cgaattgact caaatgacaa tcaaacaaga aacagaagga     240
aacataaatg aagctagacg agaagaagaa gacgaagaac aagatgaaga ttccagaaca     300
tcaatgccac ctgcattggg agaagatgat gattatgagg aggatgatgc tgatagtttt     360
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aatttaccaa atgacattgt tactggtgca tgggaaacgt acaaccacgc ggttcaacgg     480
gtttctcttg agggttcgga atcggcgtgg caactatcag caatttacta ttatcttcta     540
tcaaaaggaa taaaacgtcg tggaaaaaca atccgtattc tcattcaacc gtttcctgtt     600
tcgatactta caattgccaa ctcatttgac atatccgttg ctgaaatgct tgacaaaact     660
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gattgtacga ttattcgagc tctttgcaca caatttggtg gaagtgttct tgatgcacgg    1080
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aacaatcaaa gtctttataa tagattgaca aaaattattg gaagctggaa attggagaat    1560
tcgaaactcg aagaagtgtg tggcacaatg tccgacagtc caatggcaac aattcttctg    1620
aaaagtgatg aaatgacaaa taaattcgag cgaactttat ctgcagaact cggagagacg    1680
atcaatgaga atattcctaa atatcactat aatgttcgaa aagaattgga attagttttt    1740
ctcattttca tggagaaaat aattgttgca gaattgaaaa agaaagtacg agaggaggac    1800
ttgctgaatg tgattcgtcg ggaagaattt cttgattcag ttttctgttt ctgtgttgaa    1860
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gtacatccat ttatgtttca taaagtaatt gatttgatga taacacatga gaaacagcta    1980
agtcgtcaaa tggttcaaca ttttagtcga attgaagaaa ctgtaattga gtatttttcg    2040
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47 wt

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cattttacag ttataaaaaa aaaaaaaaa 3209

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<212> PRT
<213> Caenorhabditis elegans

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35 40 45
Asp Val Ala Lys Asp Asn Ser Asp His Thr Ile His Arg Leu Ile Leu
50 55 60
Gly Thr His Thr Ser Asp Glu Gln Asn His Leu Leu Ile Ser Lys Ile
65 70 75 80
Cys Met Pro Thr Asp Asp Ala Gln Phe Asp Ala Ser Arg Tyr Asp Thr
85 90 95
Glu Arg Ser Glu Tyr Gly Gly Phe Gly Ala Val Asn Gly Lys Val Glu
100 105 110
Pro Asp Ile Arg Ile Asn His Glu Gly Glu Val Asn Arg Ala Arg Tyr
115 120 125
Met Pro Gln Lys Ser Asn Ile Ile Ala Thr Lys Ser Pro His Ala Asp
130 135 140
Val Tyr Ile Phe Asp Tyr Leu Lys His Ser Ala Val Pro Arg Asp Asn
145 150 155 160
Thr Phe Asn Pro Leu Ile Arg Leu Lys Gly His Thr Lys Glu Gly Tyr
165 170 175
Gly Leu Ser Trp Asn Pro Asn Lys Glu Gly Leu Ile Leu Ser Ala Ser
180 185 190

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Asp Asp Gln Thr Val Cys His Trp Asp Ile Asn Ala Asn Gln Asn Val
        195                 200                 205
Ala Gly Glu Leu Gln Ala Lys Asp Val Phe Lys Gly His Glu Ser Val
    210                 215                 220
Val Glu Asp Val Ala Trp His Val Leu His Asp Gly Val Phe Gly Ser
225                 230                 235                 240
Val Gly Asp Asp Lys Lys Leu Leu Ile Trp Asp Val Arg Thr Ser Thr
                245                 250                 255
Pro Gly His Cys Ile Asp Ala His Ser Ala Glu Val Asn Cys Leu Ala
            260                 265                 270
Phe Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys
        275                 280                 285
Thr Val Ala Leu Trp Asp Leu Arg Asn Leu Arg Met Lys Leu His Ser
    290                 295                 300
Phe Glu Ser His Arg Asp Glu Ile Phe Gln Val Gln Trp Ser Pro His
305                 310                 315                 320
Asn Glu Thr Ile Leu Ala Ser Ser Gly Thr Asp Lys Arg Leu His Val
                325                 330                 335
Trp Asp Leu Ser Lys Ile Gly Glu Asp Gln Ser Ala Glu Asp Ala Glu
            340                 345                 350
Asp Gly Pro Pro Glu Leu Leu Phe Ile His Gly Gly His Thr Ala Lys
        355                 360                 365
Ile Ser Asp Phe Ser Trp Asn Pro Asn Glu Pro Trp Val Val Cys Ser
    370                 375                 380
Val Ser Glu Asp Asn Ile Leu Gln Val Trp Gln Met Ala Asp Asn Ile
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Tyr Asn Glu Val Asp Glu Glu Thr Pro Ala Asp Val Val Glu Arg Gln
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Gln
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<210> 6
<211> 1462
<212> DNA
<213> Caenorhabditis elegans

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tcactcagtg ttcaatggct cccagacgtt gcgaaggata acagcgacca tactattcat     180
cggctcattc ttggaactca tacttcagat gagcagaatc acttgcttat ttctaagatc     240
tgtatgccaa cggatgatgc ccaatttgat gcatctcgct acgataccga gcgcagtgaa     300
tacggtggtt tcggagctgt taacggaaaa gtggaacccg atattcgcat taaccacgaa     360
ggggaggtta acagagctcg ttacatgcct caaaagtcga atatcattgc tacaaagtct     420
ccacatgctg atgtttacat tttcgactat ttaaagcact ctgctgttcc tcgtgataac     480
acgttcaatc cgcttatcag actgaaagga cacacgaagg aaggctatgg attatcatgg     540
aatccaaaca aagaaggttt gattctatca gcgtcagatg atcagacagt ttgtcattgg     600
gatatcaacg caaatcagaa tgttgccggg gaattgcaag cgaaggatgt tttcaaaggt     660
cacgagtcag tcgttgaaga tgttgcttgg cacgttttgc atgatggtgt cttcggatcg     720
gttggtgacg ataagaaatt gctcatttgg gatgtgcgca caagcactcc tggacactgt     780
atcgatgctc attctgccga agttaactgt ctcgcattca atccatattc cgaattcatt     840
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ctggccaccg gatcagctga taaaactgtc gctctttggg atctacgtaa tctacgaatg 900
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aacgagacta ttcttgcatc cagcggtact gataaacgtc ttcatgtgtg ggacctatct 1020
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attcacggtg ggcacaccgc caagatcagc gatttctcgt ggaacccgaa cgagccttgg 1140
gttgtgtgca gtgtgtcaga agacaatatt ctccaagtgt ggcaaatggc tgataacata 1200
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<211> 575
<212> PRT
<213> Caenorhabditis elegans

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35 40 45
Gly Leu Arg His Phe Ser Thr Lys Val Cys Glu Lys Val Lys Glu Lys
50 55 60
Gly Leu Thr Asn Tyr Asn Glu Val Ala Asp Glu Leu Val Ala Asp Tyr
65 70 75 80
Phe Gln Asn Asn Leu Ile Lys Gln Ile Asp Val Val Lys Gln Glu Tyr
85 90 95
Asp Met Lys Asn Ile Arg Arg Arg Val Tyr Asp Ala Leu Asn Val Leu
100 105 110
Leu Ala Met Asn Ile Ile Thr Lys Ser Lys Lys Asp Ile Arg Trp Ile
115 120 125
Gly Leu Pro Ala Ser Ala Ser Gln Glu Ile Ser Arg Leu Glu Glu Glu
130 135 140
Lys Ser Arg Arg Glu Ala Ser Ile Ser Ser Lys Lys Gln Ala Leu Glu
145 150 155 160
Glu Met Val Leu Gln Ile Val Ser Tyr Lys Asn Leu Val Glu Arg Asn
165 170 175
Arg Lys Asn Glu His Lys Asn Gly Arg Pro Glu Asn Asp Thr Val Leu
180 185 190
His Leu Pro Phe Leu Ile Ile Asn Thr Asp Lys Glu Ala Asn Val Glu
195 200 205
Cys Ser Val Ser Ser Asp Lys Ser Glu Phe Leu Phe Ser Phe Asp Lys
210 215 220
Lys Phe Glu Ile His Asp Asp Phe Glu Ile Leu Lys Lys Leu Asn Leu
225 230 235 240
Ala Cys Ser Leu Glu Thr Thr Asn Pro Thr Ala Glu Glu Val Lys Thr
245 250 255
Ala Lys Ser Phe Leu Pro Thr Leu His Gln His Tyr Val Asp Glu Ile

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            260                 265                 270
Ile Ala Asn Arg Lys Lys Val Glu Ala Glu Lys Glu Glu Lys Arg Lys
        275                 280                 285
Gln Gln Gln Leu Ile Ala Asp Gln Met Ser Met Asn Leu Ser Gln Ala
    290                 295                 300
Gln Tyr Val Glu Pro Thr Ser Ser Leu Ala Gln Met Ser Tyr Ser Ser
305                 310                 315                 320
Arg Phe Asn Arg Gln Leu Gln Glu His Leu Ile Asn Asp Gly Ser Glu
                325                 330                 335
Asp Arg Ser Ala Ala Ala Gly Ile Met Glu Arg Asp Tyr Asp Met Asp
            340                 345                 350
Lys Asn Val Asn Gln Gly Ser Ala Ser Arg Gly Pro Met Tyr Asn Thr
        355                 360                 365
Tyr Ser Pro Gln Lys Ile Arg Ala Gln Val Asn Thr Pro Leu Gln Val
    370                 375                 380
Pro Pro Val Thr Lys Arg Tyr Tyr Val Gln Lys Thr Gln Gly Pro Met
385                 390                 395                 400
Lys His Asp Met Thr Pro Val Val Arg Thr Val Asn Arg Pro Tyr Ser
                405                 410                 415
Thr Val Pro Pro Asp Arg Arg Leu Ser Thr Gly Ala Thr Ser Val Asn
            420                 425                 430
Ser Gly Pro Val Lys Tyr Tyr Val Pro Gln Gly His Gln Pro Met His
        435                 440                 445
Gln Pro Val Gly Gln Arg Tyr Arg Val Arg Pro Gln Gln Pro Gln Met
    450                 455                 460
Ser His Met Gly Gln Pro His Gln Val Gln Gln Arg Val Val Tyr Pro
465                 470                 475                 480
Ala Gly Ser Ile Ser Gly His Gln Leu Gln Pro Gly Gln Arg Ile Val
                485                 490                 495
Thr Gln Arg Ile Val Ala Pro Gly Gly Pro His Pro Pro Gly Thr Ile
            500                 505                 510
Val Arg Lys Val Ile Arg Lys Ile Val Val Asn Asn Pro Lys Gln Ser
        515                 520                 525
Pro Ala Gln Gln Val Ile Gln Lys Lys Met Met Glu Gln Asp Met Cys
    530                 535                 540
Thr Phe Glu Arg Lys Thr Glu Gln Pro Met Thr Ser Ala Gln Ala Ala
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Ala Leu Ile Gln His Pro Gln Pro Glu Glu Tyr Asp Tyr Phe Gln
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<210> 8
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<212> DNA
<213> Caenorhabditis elegans

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ttcaaatgcc tacaggtctt cctcgttcat accaagatga gagtcacaat gaacctgtgg 180
gctgggatga accttcggga gttggaggat ctagtggagc aggaggtcaa caatctgaca 240
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<210> 9
<211> 324
<212> PRT
<213> Caenorhabditis elegans

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Phe Asp Glu Asp Glu Asp Leu Asp Gln Pro Gln Met Gly Thr Arg Ala
35 40 45
Asp Lys Ser Leu Gly Leu Leu Ala Lys Arg Phe Ile Arg Met Ile Gln
50 55 60
Tyr Ser Pro Tyr Gly Arg Cys Asp Leu Asn Thr Ala Ala Glu Ala Leu
65 70 75 80
Asn Val Arg Gln Lys Arg Arg Ile Tyr Asp Ile Thr Asn Val Leu Glu
85 90 95
Gly Ile Gly Leu Ile Glu Lys Arg Ser Lys Asn Met Ile Gln Trp Lys
100 105 110
Gly Gly Asp Phe Met Leu Asn Val Lys Glu Gly Lys Arg Leu Ser Ala
115 120 125
Thr Thr Glu Glu Glu Asp Arg Met Glu Gln Leu Lys Ala Glu Ile Glu
130 135 140

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Gln Leu Asn Lys Glu Glu Glu Leu Ile Glu Gln Arg Gln Arg Trp Leu
145                 150                 155                 160
Gln Gln Ser Leu Arg Asn Met Thr Glu Ser Val Glu Asn Asn Lys Leu
                165                 170                 175
Ser Tyr Val Leu Arg Ser Gln Leu Ala Glu Ile Gln Gly Ser Asp Leu
            180                 185                 190
Thr Ile Gly Ile Gln Thr Arg Val Gly Thr Gln Val Arg Leu Ser Asp
        195                 200                 205
Pro Glu Gln Val Glu Ile His Gly Gly Pro Ser Trp Cys Tyr Leu Lys
    210                 215                 220
Asp Pro Ser Gly Pro Leu Arg Ala Ala Ile Val Ser Asn His Glu Leu
225                 230                 235                 240
His Asp Phe Val Gln Arg Glu Arg Ala Lys Arg Pro Gly Glu Glu His
                245                 250                 255
Val Asp Ala Asp Ala Pro Asp Glu Met Met Asp Asp Ser Arg Tyr Arg
            260                 265                 270
Asn Arg Arg Thr Ile Asn Asp Asp Glu Met Phe Gly Phe Glu Gln Lys
        275                 280                 285
Val Pro Ala Met Lys His Leu Glu Pro Pro Pro Ala Ser Asp Asp Tyr
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Val Tyr Ser Ser Thr Gly Asp Glu Tyr Arg Gly Asp Ser Ile Val Asp
305                 310                 315                 320
Leu Tyr Gly Asp
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<210> 10
<211> 1428
<212> DNA
<213> Caenorhabditis elegans

<400> 10

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atgctcgggc tcgacaatga gcttgacttt gattttgatt ttgacgagga tgaggacctg     180
gatcaaccac aaatgggcac acgagccgat aaatcgttgg gattgttggc gaaacgattt     240
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ctcaatgtcc ggcaaaagcg acgaatctac gatattacga atgttctcga aggaattggt     360
cttattgaga aaagaagcaa gaatatgata cagtggaaag gcggtgattt tatgctaaac     420
gtgaaggaag ggaaacgact atcggccaca acagaagaag aagatcgaat ggaacaatta     480
aaagctgaaa ttgagcaatt aaataaggaa gaagagctca ttgagcaacg tcaaagatgg     540
cttcagcaga gcctccgaaa catgacagaa tccgtggaga acaacaagct cagctatgtg     600
ctccgttcac agctcgccga gattcaaggc tcagatctta cgattggaat tcaaacgaga     660
gtcggcacac aagttcggct cagtgatccg gagcaagtcg agatacacgg tggaccatct     720
tggtgttacc tgaaagatcc ctctggaccc ctccgagccg ccatcgtttc caaccatgag     780
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gccagcgatg actacgttta ttcgagcacc ggagacgagt atcgaggaga ttctatagtc    1020
gatttgtacg gagattaatt attttaatat ttttttttta aatttcgaat tctgcgacca    1080
tttctcattt gacatctatt catttactcc aaattccaaa ttttcccca aaaaaattat     1140
cgatgtttcg gctccaaatg ttattatttt cccatccaca gtgcccacac aattcataat    1200
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<210> 11
<211> 161
<212> PRT
<213> Caenorhabditis elegans

<400> 11

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Met	Phe	Val	Gln	Gln	Met	Ile	Glu	Lys	Lys	Ser	Asn	Ala	Glu	Gln	Ala
			20					25					30		
Lys	Met	Leu	Glu	Gln	Gln	Lys	Lys	Met	Leu	Glu	Cys	Thr	Glu	Thr	Met
		35					40					45			
Pro	Glu	Glu	Ser	Glu	Pro	Val	Pro	Met	Lys	Cys	Leu	Asp	Phe	Glu	Glu
	50					55					60				
Ala	Phe	Gln	Ser	Glu	Ser	Val	Ser	Lys	Gly	Tyr	Glu	Ser	Pro	Tyr	Lys
65					70					75					80
Asn	Ile	Ser	Phe	Leu	Lys	Glu	Asp	Ala	Val	Thr	Val	Asn	Thr	Met	Ser
			85						90					95	
His	Cys	Pro	Ala	Asp	Asp	Ile	Ala	Lys	Leu	Ile	Arg	Asn	Ile	Gln	Asn
		100						105					110		
Ser	Val	Tyr	Thr	Leu	Gly	Ile	Glu	Glu	Ala	Arg	Gln	Cys	Arg	Arg	Gly
	115						120					125			
Lys	Leu	Leu	Asn	Val	Leu	Lys	Pro	Thr	Gly	Ser	Ala	Ser	Pro	Arg	Tyr
	130					135					140				
Leu	Gln	Pro	Thr	Pro	Pro	Lys	Asn	Val	Ala	Glu	Glu	Thr	Thr	Gly	Ser
145					150					155					160
Gln															

<210> 12
<211> 493
<212> DNA
<213> Caenorhabditis elegans

<400> 12
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atgctcgaat gcaccgaaac aatgccagaa gaaagtgagc cagttccaat gaaatgtctc 180
gattttgaag aagcatttca aagcgaatca gtatcaaaag gttacgaatc gccatacaag 240
aatatttcgt ttctcaagga agatgctgtg actgttaata caatgagcca ctgcccagcc 300
gacgatatcg ccaagctcat ccgaaacatt caaaactcgg tgtacactct tggaatcgaa 360
gaagctcgcc agtgccgacg tggaaagttg ctcaacgtgc tgaaacccac tggctcggct 420
tctccgagat atttgcagcc aacaccaccg aaaaatgtag cggaagaaac gacaggaagc 480
cagtgaaatt gaa 493

<210> 13

<211> 438
<212> PRT
<213> Caenorhabditis elegans

<400> 13

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            20                  25                  30
Val Asn Gly Gln Leu Val Pro His Asn Pro Asn Leu Gln Ala Gln Gln
        35                  40                  45
Asn Arg Pro Gly Thr Ser Ser Met Ile Gln Gln His Asn Arg Ser Met
    50                  55                  60
Glu Val Asn Gln Gly Leu Val Lys Asp Glu Pro Ile Asp Thr Ser Ser
65                  70                  75                  80
His Arg Val Tyr Val Pro Pro Pro Arg Pro Val Gln Arg Lys Leu Trp
                85                  90                  95
Lys Leu Phe Gln Pro Gly Pro Ser Thr Pro Gly Ser Ser Gln Tyr Thr
            100                 105                 110
Val Arg Asn Leu Ser Asn Leu Ser Gly Ser Pro Ser Met Tyr Asp Arg
        115                 120                 125
Gln Pro Ala Ser Leu Pro Arg Thr Val Gln Pro Met Gly Leu Glu Met
    130                 135                 140
Gly Asn Ser Glu Gln Arg Lys Val Tyr Ile Asp Met Lys Asp His Val
145                 150                 155                 160
Ser His Ile Arg Leu Lys Thr Lys Lys Lys Val Phe Ala Pro Gly Gln
                165                 170                 175
Arg Lys Pro Cys Asn Cys Thr Lys Ser Gln Cys Leu Lys Leu Tyr Cys
            180                 185                 190
Asp Cys Phe Ala Asn Gly Glu Phe Cys Arg Asp Cys Asn Cys Lys Asp
        195                 200                 205
Cys His Asn Asn Ile Glu Tyr Asp Ser Gln Arg Ser Lys Ala Ile Arg
    210                 215                 220
Gln Ser Leu Glu Arg Asn Pro Asn Ala Phe Lys Pro Lys Ile Gly Ile
225                 230                 235                 240
Ala Arg Gly Gly Ile Thr Asp Ile Glu Arg Leu His Gln Lys Gly Cys
                245                 250                 255
His Cys Lys Lys Ser Gly Cys Leu Lys Asn Tyr Cys Glu Cys Tyr Glu
            260                 265                 270
Ala Lys Val Pro Cys Thr Asp Arg Cys Lys Cys Lys Gly Cys Gln Asn
        275                 280                 285
Thr Glu Thr Tyr Arg Met Thr Arg Tyr Lys Asn Ser Gly Gly Ala Val
    290                 295                 300
Ser Asn Thr Asn Ala Leu Met Ser Leu Thr Asn Ala Ser Ser Thr Ala
305                 310                 315                 320
Thr Pro Asp Ser Gly Pro Gly Ser Val Val Thr Asp Glu His Gly Asp
                325                 330                 335
Asp Tyr Glu Asp Met Leu Leu Ser His Lys Pro Lys Val Glu Met Asp
            340                 345                 350
Pro Arg Arg Phe Pro Trp Tyr Tyr Met Thr Asp Glu Val Val Glu Ala
        355                 360                 365
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Ala Thr Met Cys Met Val Ala Gln Ala Glu Glu Ala Leu Asn Tyr Glu
    370                 375                 380
Lys Val Gln Thr Glu Asp Glu Lys Leu Ile Asn Met Glu Lys Leu Val
385                 390                 395                 400
Leu Arg Glu Phe Gly Arg Cys Leu Glu Gln Met Ile Thr Asn Thr Thr
                405                 410                 415
Glu Leu Thr Gln Asp Leu Asp Ala Ala Pro Thr Asp Asp Ile Pro Gly
            420                 425                 430
Pro Ser Thr Ser Thr Ser
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<210> 14
<211> 1503
<212> DNA
<213> Caenorhabditis elegans

<400> 14

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acagcttgtg cctcataatc caaacttaca ggcgcagcaa aatcgtccgg gaacctcgag     180
tatgattcaa cagcataatc gatcaatgga agttaatcag ggattggtca aagacgaacc     240
aattgataca tcatcgcatc gcgtctacgt ccccccctccg agaccagttc agcgaaaact     300
ttggaagctt tttcagcctg ggcccagcac tcccggatcg tctcagtaca ctgtgcggaa     360
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aacagtgcaa ccaatgggct tggagatggg aaattctgaa cagcgaaaag tttacatcga     480
tatgaaagat cacgttagtc atattagatt gaaaactaaa aaaaaagtat ttgcacctgg     540
ccagcggaaa ccatgcaatt gcacgaaatc tcaatgcctc aagctctact gtgattgttt     600
cgccaatgga gagttctgtc gtgactgcaa ttgcaaggat tgtcacaata atatagaata     660
cgacagtcag cgttcaaaag ccatccgtca gtcacttgag cgaaatccga acgctttcaa     720
gccaaaaatt ggtattgctc gtggaggtat taccgacatc gaacgtcttc atcagaaagg     780
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tccgtgtacc gatcgatgca agtgcaaagg atgtcagaat actgaaacat acagaatgac     900
aagatacaag aactccggtg gtgccgtgtc caatacgaat gccctgatgt cattgaccaa     960
cgcttccagc acagcgactc cagattctgg tccgggaagt gtggtgaccg atgagcatgg    1020
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cttcccgtgg tactatatga ccgatgaagt cgttgaggca gccactatgt gcatggttgc    1140
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tatggagaag cttgtccttc gtgaattcgg ccgctgtctc gaacaaatga tcacaaacac    1260
aactgagctc acacaagatc ttgatgccgc tccaacggat gacatcccag gaccatctac    1320
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cat                                                                  1503
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<210> 15
<211> 449
<212> DNA
<213> Mus musculus

<400> 15

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<210> 16
<211> 3535
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(3535)
<223> n = A,T,C or G

<400> 16
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<210> 17
<211> 30
<212> PRT
<213> Caenorhabditis elegans

<220>

<221> VARIANT
<222> (1)...(30)
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Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Cys Xaa Xaa Cys
            20   25   30

<210> 18
<211> 31
<212> PRT
<213> Caenorhabditis elegans

<220>

<221> VARIANT
<222> (1)...(31)
<223> Xaa = Any Amino Acid other than Cys

<400> 18

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Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Cys
            20                  25                  30
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